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09753385

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RAW SEQUENCE LISTING

DATE: 12/31/2002

PATENT APPLICATION: US/09/753,385

TIME: 14:15:22

Input Set : A:\10278-025004.TXT

Output Set: N:\CRF4\12312002\I753385.raw

C--> 4 <110> APPLICANT: Heartlein, Michael W.
 5 Lemontt, Jeffrey F.
 6 Concino, Michael F.
 8 <120> TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE IN TRANSPORT
 9 OF A SELECTED SUBSTANCE INTO CELLS
 12 <130> FILE REFERENCE: 10278-025004
 14 <140> CURRENT APPLICATION NUMBER: US 09/753,385
 15 <141> CURRENT FILING DATE: 2002-12-10
 17 <150> PRIOR APPLICATION NUMBER: US 08/470,058
 18 <151> PRIOR FILING DATE: 1995-06-06
 20 <150> PRIOR APPLICATION NUMBER: US 09/037,188
 21 <151> PRIOR FILING DATE: 1998-03-09
 23 <150> PRIOR APPLICATION NUMBER: US 09/285,310
 24 <151> PRIOR FILING DATE: 1999-04-02
 26 <160> NUMBER OF SEQ ID NOS: 12
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 3428
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (14)...(3235)
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42	1 5 10	
44	gcc ttg ctc ctc gcc gcg gcg ggg act gca gtg ggc gac aga tgt gaa	97
45	Ala Leu Leu Leu Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu	
46	15 20 25	
48	aga aac gag ttc cag tgc caa gac ggg aaa tgc atc tcc tac aag tgg	145
49	Arg Asn Glu Phe Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp	
50	30 35 40	
52	gtc tgc gat ggc agc gct gag tgc cag gat ggc tct gat gag tcc cag	193
53	Val Cys Asp Gly Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln	
54	45 50 55 60	
56	gag acg tgc ttg tct gtc acc tgc aaa tcc ggg gac ttc agc tgt ggg	241
57	Glu Thr Cys Leu Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly	
58	65 70 75	
60	ggc cgt gtc aac cgc tgc att cct cag ttc tgg agg tgc gat ggc caa	289
61	Gly Arg Val Asn Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln	
62	80 85 90	
64	gtg gac tgc gac aac ggc tca gac gag caa ggc tgt ccc ccc aag acg	337

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65	Val	Asp	Cys	Asp	Asn	Gly	Ser	Asp	Glu	Gln	Gly	Cys	Pro	Pro	Lys	Thr	
66			95					100				105					
68	tgc	tcc	cag	gac	gag	ttt	cgc	tgc	cac	gat	ggg	aag	tgc	atc	tct	cgg	385
69	Cys	Ser	Gln	Asp	Glu	Phe	Arg	Cys	His	Asp	Gly	Lys	Cys	Ile	Ser	Arg	
70		110					115					120					
72	cag	ttc	gtc	tgt	gac	tca	gac	cgg	gac	tgc	ttg	gac	ggc	tca	gac	gag	433
73	Gln	Phe	Val	Cys	Asp	Ser	Asp	Arg	Asp	Cys	Leu	Asp	Gly	Ser	Asp	Glu	
74	125					130					135					140	
76	gcc	tcc	tgc	ccg	gtg	ctc	acc	tgt	ggg	ccc	gcc	agc	ttc	cag	tgc	aac	481
77	Ala	Ser	Cys	Pro	Val	Leu	Thr	Cys	Gly	Pro	Ala	Ser	Phe	Gln	Cys	Asn	
78					145					150					155		
80	agc	tcc	acc	tgc	atc	ccc	cag	ctg	tgg	gcc	tgc	gac	aac	gac	ccc	gac	529
81	Ser	Ser	Thr	Cys	Ile	Pro	Gln	Leu	Trp	Ala	Cys	Asp	Asn	Asp	Pro	Asp	
82			160						165				170				
84	tgc	gaa	gat	ggc	tcg	gat	gag	tgg	ccg	cag	cgc	tgt	agg	ggg	ctt	tac	577
85	Cys	Glu	Asp	Gly	Ser	Asp	Glu	Trp	Pro	Gln	Arg	Cys	Arg	Gly	Leu	Tyr	
86		175					180					185					
88	gtg	ttc	caa	ggg	gac	agt	agc	ccc	tgc	tcg	gcc	ttc	gag	ttc	cac	tgc	625
89	Val	Phe	Gln	Gly	Asp	Ser	Ser	Pro	Cys	Ser	Ala	Phe	Glu	Phe	His	Cys	
90		190					195					200					
92	cta	agt	ggc	gag	tgc	atc	cac	tcc	agc	tgg	cgc	tgt	gat	ggg	ggc	ccc	673
93	Leu	Ser	Gly	Glu	Cys	Ile	His	Ser	Ser	Trp	Arg	Cys	Asp	Gly	Gly	Pro	
94	205					210					215					220	
96	gac	tgc	aag	gac	aaa	tct	gac	gag	gaa	aac	tgc	gct	gtg	gcc	acc	tgt	721
97	Asp	Cys	Lys	Asp	Lys	Ser	Asp	Glu	Glu	Asn	Cys	Ala	Val	Ala	Thr	Cys	
98				225					230				235				
100	cgc	cct	gac	gaa	ttc	cag	tgc	tct	gat	gga	aac	tgc	atc	cat	ggc	agc	769
101	Arg	Pro	Asp	Glu	Phe	Gln	Cys	Ser	Asp	Gly	Asn	Cys	Ile	His	Gly	Ser	
102			240						245				250				
104	cgg	cag	tgt	gac	cgg	gaa	tat	gac	tgc	aag	gac	atg	agc	gat	gaa	gtt	817
105	Arg	Gln	Cys	Asp	Arg	Glu	Tyr	Asp	Cys	Lys	Asp	Met	Ser	Asp	Glu	Val	
106			255					260				265					
108	ggc	tgc	gtt	aat	gtg	aca	ctc	tgc	gag	gga	ccc	aac	aag	ttc	aag	tgt	865
109	Gly	Cys	Val	Asn	Val	Thr	Leu	Cys	Glu	Gly	Pro	Asn	Lys	Phe	Lys	Cys	
110		270					275					280					
112	cac	agc	ggc	gaa	tgc	atc	acc	ctg	gac	aaa	gtc	tgc	aac	atg	gct	aga	913
113	His	Ser	Gly	Glu	Cys	Ile	Thr	Leu	Asp	Lys	Val	Cys	Asn	Met	Ala	Arg	
114	285					290					295					300	
116	gac	tgc	cgg	gac	tgg	tca	gat	gaa	ccc	atc	aaa	gag	tgc	ggg	acc	aac	961
117	Asp	Cys	Arg	Asp	Trp	Ser	Asp	Glu	Pro	Ile	Lys	Glu	Cys	Gly	Thr	Asn	
118				305						310				315			
120	gaa	tgc	ttg	gac	aac	aac	ggc	ggc	tgt	tcc	cac	gtc	tgc	aat	gac	ctt	1009
121	Glu	Cys	Leu	Asp	Asn	Asn	Gly	Gly	Cys	Ser	His	Val	Cys	Asn	Asp	Leu	
122				320					325				330				
124	aag	atc	ggc	tac	gag	tgc	ctg	tgc	ccc	gac	ggc	ttc	cag	ctg	gtg	gcc	1057
125	Lys	Ile	Gly	Tyr	Glu	Cys	Leu	Cys	Pro	Asp	Gly	Phe	Gln	Leu	Val	Ala	
126			335					340				345					
128	cag	cga	aga	tgc	gaa	gat	atc	gat	gag	tgt	cag	gat	ccc	gac	acc	tgc	1105
129	Gln	Arg	Arg	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Gln	Asp	Pro	Asp	Thr	Cys	

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130	350	355	360	
132	agc cag ctc tgc gtg aac ctg gag ggt ggc tac aag tgc cag tgt gag	1153		
133	Ser Gln Leu Cys Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu			
134	365 370 375 380			
136	gaa ggc ttc cag ctg gac ccc cac acg aag gcc tgc aag gct gtg gtc	1201		
137	Glu Gly Phe Gln Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Val			
138	385 390 395			
140	cct gat aaa act gtg aga tgg tgt gca gtg tcg gag cat gag gcc act	1249		
141	Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu His Glu Ala Thr			
142	400 405 410			
144	aag tgc cag agt ttc cgc gac cat atg aaa agc gtc att cca tcc gat	1297		
145	Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val Ile Pro Ser Asp			
146	415 420 425			
148	ggg ccc agt gtt gct tgt gtg aag aaa gcc tcc tac ctt gat tgc atc	1345		
149	Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr Leu Asp Cys Ile			
150	430 435 440			
152	agg gcc att gcg gca aac gaa gcg gat gct gtg aca ctg gat gca ggt	1393		
153	Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr Leu Asp Ala Gly			
154	445 450 455 460			
156	ttg gtg tat gat gct tac ttg gct ccc aat aac ctg aag cct gtg gtg	1441		
157	Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu Lys Pro Val Val			
158	465 470 475			
160	gca gag ttc tat ggg tca aaa gag gat cca cag act ttc tat tat gct	1489		
161	Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr Phe Tyr Tyr Ala			
162	480 485 490			
164	gtt gct gtg gtg aag aag gat agt ggc ttc cag atg aac cag ctt cga	1537		
165	Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met Asn Gln Leu Arg			
166	495 500 505			
168	ggc aag aag tcc tgc cac acg ggt cta ggc agg tcc gct ggg tgg aac	1585		
169	Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser Ala Gly Trp Asn			
170	510 515 520			
172	atc ccc ata ggc tta ctt tac tgt gac tta cct gag cca cgt aaa cct	1633		
173	Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu Pro Arg Lys Pro			
174	525 530 535 540			
176	ctt gag aaa gca gtg gcc aat ttc ttc tcg ggc agc tgt gcc cct tgt	1681		
177	Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser Cys Ala Pro Cys			
178	545 550 555			
180	gcg gat ggg acg gac ttc ccc cag ctg tgt caa ctg tgt cca ggg tgt	1729		
181	Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu Cys Pro Gly Cys			
182	560 565 570			
184	ggc tgc tcc acc ctt aac caa tac ttc ggc tac tcg gga gcc ttc aag	1777		
185	Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser Gly Ala Phe Lys			
186	575 580 585			
188	tgt ctg aag gat ggt gct ggg gat gtg gcc ttt gtc aag cac tcg act	1825		
189	Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val Lys His Ser Thr			
190	590 595 600			
192	ata ttt gag aac ttg gca aac aag gct gac agg gac cag tat gag ctg	1873		
193	Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp Gln Tyr Glu Leu			
194	605 610 615 620			

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196	ctt	tgc	cta	gac	aac	acc	cgg	aag	ccg	gta	gat	gaa	tac	aag	gac	tgc	1921
197	Leu	Cys	Leu	Asp	Asn	Thr	Arg	Lys	Pro	Val	Asp	Glu	Tyr	Lys	Asp	Cys	
198				625						630					635		
200	cac	ttg	gcc	cag	gtc	cct	tct	cat	acc	gtc	gtg	gcc	cga	agt	atg	ggc	1969
201	His	Leu	Ala	Gln	Val	Pro	Ser	His	Thr	Val	Val	Ala	Arg	Ser	Met	Gly	
202				640						645					650		
204	ggc	aag	gag	gac	ttg	atc	tgg	gag	ctt	ctc	aac	cag	gcc	cag	gaa	cat	2017
205	Gly	Lys	Glu	Asp	Leu	Ile	Trp	Glu	Leu	Leu	Asn	Gln	Ala	Gln	Glu	His	
206				655						660					665		
208	ttt	ggc	aaa	gac	aaa	tca	aaa	gaa	ttc	caa	cta	ttc	agc	tct	cct	cat	2065
209	Phe	Gly	Lys	Asp	Lys	Ser		Glu	Phe	Gln	Leu	Phe	Ser	Ser	Pro	His	
210				670						675					680		
212	ggg	aag	gac	ctg	ctg	ttt	aag	gac	tct	gcc	cac	ggg	ttt	tta	aaa	gtc	2113
213	Gly	Lys	Asp	Leu	Leu	Phe	Lys	Asp	Ser	Ala	His	Gly	Phe	Leu	Lys	Val	
214	685					690						695				700	
216	ccc	cca	agg	atg	gat	gcc	aag	atg	tac	ctg	ggc	tat	gag	tat	gtc	act	2161
217	Pro	Pro	Arg	Met	Asp	Ala	Lys	Met	Tyr	Leu	Gly	Tyr	Glu	Tyr	Val	Thr	
218				705						710					715		
220	gcc	atc	cgg	aat	cta	cgg	gaa	ggc	aca	tgc	cca	gaa	gcc	cca	aca	gat	2209
221	Ala	Ile	Arg	Asn	Leu	Arg	Glu	Gly	Thr	Cys	Pro	Glu	Ala	Pro	Thr	Asp	
222				720						725					730		
224	gaa	tgc	aag	cct	gtg	aag	tgg	tgt	gcg	ctg	agc	cac	cac	gag	agg	ctc	2257
225	Glu	Cys	Lys	Pro	Val	Lys	Trp	Cys	Ala	Leu	Ser	His	His	Glu	Arg	Leu	
226				735						740					745		
228	aag	tgt	gat	gag	tgg	agt	gtt	aac	agt	gta	ggg	aaa	ata	gag	tgt	gta	2305
229	Lys	Cys	Asp	Glu	Trp	Ser	Val	Asn	Ser	Val	Gly	Lys	Ile	Glu	Cys	Val	
230				750						755					760		
232	tca	gca	gag	acc	acc	gaa	gac	tgc	atc	gcc	aag	atc	atg	aat	gga	gaa	2353
233	Ser	Ala	Glu	Thr	Thr	Glu	Asp	Cys	Ile	Ala	Lys	Ile	Met	Asn	Gly	Glu	
234	765					770						775				780	
236	gct	gat	gcc	atg	agc	ttg	gat	gga	ggg	ttt	gtc	tac	ata	gcg	ggc	aag	2401
237	Ala	Asp	Ala	Met	Ser	Leu	Asp	Gly	Gly	Phe	Val	Tyr	Ile	Ala	Gly	Lys	
238				785						790					795		
240	tgt	ggt	ctg	gtg	cct	gtc	ttg	gca	gaa	aac	tac	aat	aag	agc	gat	aat	2449
241	Cys	Gly	Leu	Val	Pro	Val	Leu	Ala	Glu	Asn	Tyr	Asn	Lys	Ser	Asp	Asn	
242				800						805					810		
244	tgt	gag	gat	aca	cca	gag	gca	ggg	tat	ttt	gct	gta	gca	gtg	gtg	aag	2497
245	Cys	Glu	Asp	Thr	Pro	Glu	Ala	Gly	Tyr	Phe	Ala	Val	Ala	Val	Val	Lys	
246				815						820					825		
248	aaa	tca	gct	tct	gac	ctc	acc	tgg	gac	aat	ctg	aaa	ggc	aag	aag	tcc	2545
249	Lys	Ser	Ala	Ser	Asp	Leu	Thr	Trp	Asp	Asn	Leu	Lys	Gly	Lys	Lys	Ser	
250				830						835					840		
252	tgc	cat	acg	gca	gtt	ggc	aga	acc	gct	ggc	tgg	aac	atc	ccc	atg	ggc	2593
253	Cys	His	Thr	Ala	Val	Gly	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly	
254	845					850						855				860	
256	ctg	ctc	tac	aat	aag	atc	aac	cac	tgc	aga	ttt	gat	gaa	ttt	ttc	agt	2641
257	Leu	Leu	Tyr	Asn	Lys	Ile	Asn	His	Cys	Arg	Phe	Asp	Glu	Phe	Phe	Ser	
258				865						870					875		
260	gaa	ggt	tgt	gcc	cct	ggg	tct	aag	aaa	gac	tcc	agt	ctc	tgt	aag	ctg	2689

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264 tgt atg ggc tca ggc cta aac ctg tgt gaa ccc aac aac aaa gag gga      2737
265 Cys Met Gly Ser Gly Leu Asn Leu Cys Glu Pro Asn Asn Lys Glu Gly
266      895      900      905
268 tac tac ggc tac aca ggc gct ttc agg tgt ctg gtt gag aag gga gat      2785
269 Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val Glu Lys Gly Asp
270      910      915      920
272 gtg gcc ttt gtg aaa cac cag act gtc cca cag aac act ggg gga aaa      2833
273 Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn Thr Gly Gly Lys
274 925      930      935      940
276 aac cct gat cca tgg gct aag aat ctg aat gaa aaa gac tat gag ttg      2881
277 Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys Asp Tyr Glu Leu
278      945      950      955
280 ctg tgc ctt gat ggt acc agg aaa cct gtg gag gag tat gcg aac tgc      2929
281 Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu Tyr Ala Asn Cys
282      960      965      970
284 cac ctg gcc aga gcc ccg aat cac gct gtg gtc aca cgg aaa gat aag      2977
285 His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr Arg Lys Asp Lys
286      975      980      985
288 gaa gct tgc gtc cac aag ata tta cgt caa cag cag cac cta ttt gga      3025
289 Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln His Leu Phe Gly
290      990      995      1000
292 agc aac gta act gac tgc tcg ggc aac ttt tgt ttg ttc cgg tcg gaa      3073
293 Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu Phe Arg Ser Glu
294 1005      1010      1015      1020
296 acc aag gac ctt ctg ttc aga gat gac aca gta tgt ttg gcc aaa ctt      3121
297 Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys Leu Ala Lys Leu
298      1025      1030      1035
300 cat gac aga aac aca tat gaa aaa tac tta gga gaa gaa tat gtc aag      3169
301 His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu Glu Tyr Val Lys
302      1040      1045      1050
304 gct gtt ggt aac ctg aga aaa tgc tcc acc tca tca ctc ctg gaa gcc      3217
305 Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser Leu Leu Glu Ala
306      1055      1060      1065
308 tgc act ttc cgt aga cct taaaatctca gaggtagggc tgccaccaag      3265
309 Cys Thr Phe Arg Arg Pro
310      1070
312 gtgaagatgg gaacgcagat gatccatgag tttgccctgg tttcactggc ccaagtgggt      3325
313 tgtgtctaacc acgtctgtct tcacagctct gtgttgccat gtgtgctgaa caaaaaataa      3385
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319 <213> ORGANISM: Homo sapiens
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VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date